Remarks

Claims 1-7, 13-20, 26-29, 31-34, 36, and 37 are under examination in the present application. Claim 27 has been rejected under 35 USC §112, second paragraph and 35 USC §101. Claims 1-7, 13-20, 26-29, 31-34, 36, and 37 have been rejected under 35 USC §103 (a) over Neville, US Pub. No. 2005/0196771 and Koleszar, USPNo. 6,519,583.

Applicants have amended claims 1, 14, and 27 and have cancelled claims 28 and 33. The substance of claims 28 and 33 has been included into the independent claims. The support for color coding of calls that was included into claims 1, 14 and 27 is supported at page 38, lines 8-27 and Fig. 4b. Support for the analysis of multiple samples is shown at page 38, lines 8-15.

Rejections under 35 USC §112, second paragraph and 35 USC §101

Applicants have amended claim 27 to overcome the rejections under 35 USC §112, second paragraph and 35 USC §101. They have amended the claim to recite only one statutory class. Therefore, they request that that Examiner reconsider and withdraw the §112 and §101 rejections.

Rejection based on 35 USC §103

The present invention relates to identifying the genotype differences between multiple individuals using probe array data and displaying those differences in a coded fashion in a GUI. The Koleszar prior art reference takes static annotation from the literature or databases for display. It does not take data of an array experiment and analyze it using the presently claimed series of panes and GUIs.

Applicants have also amended the claims to add additional limitations to overcome Neville, US Pub. No. 2005/0196771 and Koleszar, USPNo. 6,519,583 references. They specify that the sequence from either of the three panes be color coded to show a heterozygous call, a homozygous call, and no call. Furthermore, the present claims also specify that sequences from multiple samples be analyzed in the multiple

panes. Applicants believe that neither reference individually shows the new amended claims, nor does the combination show the newly claimed invention.

The use of color coding is advantageous in the present invention in viewing the sequence in any of the three panes because it allows a quick view of a stretch of sequence which has a SNP to be quickly identified without looking at all of the bases individually. Viewing at a high level does not immediately identify the specific SNP, but allows the user to locate the area of interest, zoom in to identify the SNP, and to investigate the sequence more fully. Color coding facilitates the quick identification of the area for the specific SNP sequence at a high level and then the user can zoom in to look at the more specific sequence. Thus, the invention allows for quick and accurate analysis of DNA sequence through the graphical user interface. Consequently, Applicants believe that they have defined a novel invention over that shown in either of the two references.

The Examiner asserts that Neville shows genotyping calls in one, two or three panes (See fig. 7 and 12 a-j). Applicant respectfully disagree. Figures 7 and 12 show that they are not panes as recited in Applicants claims. They are just patent drawings to represent some information. For example, Figs. 7 and 12 show a table of oligonucleotide probes or targets. In sum, none of these figures shows a GUI or even one, two or three panes in a GUI. Consequently, Applicants respectfully request that the Examiner reconsider and withdraw the present rejection.

Neville has disclosure of the use of color with respect to the use of an Invader assay (paragraph 158), in which colors are shown for calls in a plate. Neville does not relate to a probe array experiment, display in a GUI, multiple panes in the GUI for differential display, or the relationship between the first, second, and third panes and the sequences therein. It does not allow the use of a dynamic analysis, like zooming, to identify a sequence of interest and to go from a high level sequence overview to a more specific in-depth look. Claim 1 specifically recites the use of a GUI and panes coupled with the color coding as follows:

> displaying a plurality of the genotype calls of each of the genotype data sets to a user in a graphical user interface comprising a first pane that displays a graphical representation of a first region of sequence associated

with the genotype data sets, a second pane that displays a graphical representation of a second region of sequence selected from the first region of sequence, and a third pane that displays a graphical representation of a third region of sequence selected from the second region of sequence, wherein the graphical representation of the second region includes greater detail than the graphical representation of the first region, the graphical representation of the third region includes greater detail then the graphical representation of the second region and comprises a representation of sequence composition including the one or more genotype calls of each genotype data set; and

color coding the displayed sequences from a plurality of different samples in the first, second, or third panes to identify a plurality of calls, consisting of heterozygous calls, homozygous calls, and no calls.

Neville does not show the above invention.

In addition to the discussion above, Applicants assert that there is no motivation to combine Koleszar and Neville to obtain Applicant's presently claimed invention. For example, Koleszar is focused on analyzing one sequence at a time in varying levels of scrutiny. They do not analyze multiple samples, but simply compare sequence information to static information taken from the literature or databases. Neville is interested in multiple variants of one type of gene. They do not show or suggest varying ways to portray the information in the same manner as claimed. Therefore, Applicants suggest that one of ordinary skill in the art would not look to the combination of Koleszar and Neville for the presently claimed invention which analyzes probe array results from multiple different samples in three levels of panes in a GUI to identify color coded genotyping calls.

Conclusion

Applicants have addressed the rejection under 35 USC §112, second paragraph and 35 USC §101 by amending claim 27 to recite one statutory class. Additionally, Applicants have addressed the rejection under 35 USC §103 by amending the claims to include the limitation of color coding the SNP call. Consequently, Applicants respectfully request that the Examiner reconsider and withdraw the present rejections.

Applicants believe that no fee is required. However, if a fee is required, the Commissioner is hereby authorized to deduct such fee from the undersigned's Deposit Account, 01-0431.

Respectfully submitted,

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Date: April 10, 2007

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